

00000000-0000-0000-0000-000000000000

## Sequence listing

### (1) GENERAL INFORMATION:

#### (i) APPLICANT:

- (A) NAME: Medeva Europe Limited
- (B) STREET: 10 St James's Street
- (C) CITY: London
- (D) STATE: not applicable
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): SW1A 1EF

(ii) TITLE OF INVENTION: VACCINES CONTAINING ATTENUATED BACTERIA

(iii) NUMBER OF SEQUENCES: 4

#### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

### *Seq 2-* (2) INFORMATION FOR SEQ ID NO: 1:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

#### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1281

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GCG AAT Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn	48
1 5 10 15	
ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCG GTC GTC Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val	96
20 25 30	
AAT AAT GGC GTC GTG CTG GAA AGC GAC GTT GAT GGC TTA ATG CAA TCA Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser	144
35 40 45	

GTC AAA CTC AAC GCG GGT CAG GCA GGT CAG CAG CTT CCG GAC GAC GCC Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala	192
50 55 60	
ACG CTG CGT CAC CAG ATC CTG GAA CGT TTG ATT ATG GAT CAA ATT ATC Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile	240
65 70 75 80	
CTG CAG ATG GGT CAG AAG ATG GGG GTG AAG ATC ACG GAT GAG CAG TTG Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu	288
85 90 95	
GAT CAG CCA TCA GCC AAC ATC GCC AAA CAA AAC AAT ATG ACG ATG GAT Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp	336
100 105 110	
CAG ATG CGC AGC CGT CTG GCT TAC GAT GGG CTG AAC TAT TCA ACC TAC Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr	384
115 120 125	
CGT AAC CAG ATT CGT AAA GAG ATG ATT ATC TCT GAA GTG CGC AAC AAT Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn	432
130 135 140	
GAG GTT CGT CGC CGT ATC ACC GTT TTG CCG CAA GAA GTT GAC GCG CTG Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu	480
145 150 155 160	
GCA AAA CAG ATT GGC ACC CAA AAC GAT GCG AGC ACC GAG CTG AAC CTG Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu	528
165 170 175	
AGC CAT ATC CTG ATT GCT CTG CCG GAA AAC CCA ACC TCC GAG CAG GTT Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val	576
180 185 190	
AAC GAC GCG CAG CGC CAG GCG GAA AGC ATT GTT GAA GAA GCG CGT AAC Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn	624
195 200 205	
GGC GCA GAT TTC GGC AAA CTG GCG ATT ACC TAC TCT GCC GAC CAG CAG Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln	672
210 215 220	
GCG CTA AAA GGC GGT CAG ATG GGC TGG GGC CGT ATC CAG GAG CTG CCG Ala Leu Lys Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro	720
225 230 235 240	
GGG ATT TTC GCC CAG GCG CTG AGC ACC GCG AAG AAA GGC GAC ATT GTC Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val	768
245 250 255	
GGC CCG ATT CGC TCC GGC GTC TTC CAC ATT CTG AAA GTA AAT GAC Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp	816
260 265 270	

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CTG CGC GGT CAG AGC CAG AGT ATC TCC GTG ACC GAA GTT CAC GCT CGT Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val Val His Ala Arg 275 280 285	864
CAC ATT CTG CTT AAG CCG TCG CCG ATC ATG AAC GAT CAG CAG GCG CGC His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg 290 295 300	912
CTG AAG CTG GAA GAA ATC GCG GCT GAC ATT AAG AGT GGT AAA ACC ACC Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr 305 310 315 320	960
TTT GCC GCT GCG GCG AAA GAG TAC TCT CAG GAC CCG GGC TCC GCT AAC Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn 325 330 335	1008
CAG GGC GGT GAT TTG GGT TGG GCT ACG CCA GAT ATT TTC GAC CCG GCG Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala 340 345 350	1056
TTC CGC GAC GCG CTA ACG AAG CTG CAT AAA GGC CAA ATA AGC GCG CCG Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro 355 360 365	1104
GTA CAC TCC TCT TTC GGC TGG CAT CTG ATC GAA TTG CTG GAT ACG CGT Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg 370 375 380	1152
AAG GTA GAC AAA ACC GAT GCG GCG CAG AAA GAT CGC GCT TAT CGT ATG Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met 385 390 395 400	1200
CTG ATG AAC CGT AAA TTC TCA GAA GAA GCG GCG ACC TGG ATG CAA GAA Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu 405 410 415	1248
CAG CGC GCC ACT TAC GTT AAG ATT TTG AGT AAC TAATGA Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn 420 425	1287

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn  
1 5 10 15

Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val

20                  25                  30

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser  
35                  40                  45

Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala  
50                  55                  60

Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile  
65                  70                  75                  80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu  
85                  90                  95

Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp  
100                105                110

Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr  
115                120                125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn  
130                135                140

Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu  
145                150                155                160

Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu  
165                170                175

Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val  
180                185                190

Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn  
195                200                205

Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln  
210                215                220

Ala Leu Lys Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro  
225                230                235                240

Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val  
245                250                255

Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp  
260                265                270

Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg  
275                280                285

His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg  
290                295                300

Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr  
305                310                315                320

Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn  
 325 330 335  
 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala  
 340 345 350  
 Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro  
 355 360 365  
 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg  
 370 375 380  
 Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met  
 385 390 395 400  
 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu  
 405 410 415  
 Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn  
 420 425

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1287 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: E.coli
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GGG AAT 48  
 Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn  
 430 435 440

ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCC GTC GTC 96  
 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val  
 445 450 455

AAT AAC GGC GTC GTG CTG GAA AGC GAC GTT GAT GGA TTA ATG CAG TCG 144  
 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser  
 460 465 470 475

GTA AAA CTG AAC GCT GCT CAG GCA AGG CAG CAA CTT CCT GAT GAC GCG 192  
 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala

095044200000

Seeds

480	485	490	
ACG CTG CGC CAC CAA ATC ATG GAA CGT TTG ATC ATG GAT CAA ATC ATT Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile	495	500	240
CTG CAG ATG GGG CAG AAA ATG GGA GTG AAA ATC TCC GAT GAG CAG CTG Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu	510	515	288
GAT CAG GGG ATT GCT AAC ATC GCG AAA CAG AAC AAC ATG ACG CTG GAT Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp	525	530	336
CAG ATG CGC AGC CGT CTG GCT TAC GAT GGA CTG AAC TAC AAC ACC TAT Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr	540	545	384
CGT AAC CAG ATC CGC AAA GAG ATG ATT ATC TCT GAA GTG CGT AAC AAC Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn	560	565	432
GAG GTG CGT CGC ATC ACC ATC CTG CCG CAG GAA GTC GAA TCC CTG Glu Val Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu	575	580	480
GCG CAG CAG GTG GGT AAC CAA AAC GAC GCC AGC ACT GAG CTG AAC CTG Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu	590	595	528
AGC CAC ATC CTG ATC CCG CTG CCG GAA AAC CCG ACC TCT GAT CAG GTG Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val	605	610	576
AAC GAA GCG GAA AGC CAG GCG CGC GCC ATT GTC GAT CAG GCG CGT AAC Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn	620	625	624
GGC GCT GAT TTC GGT AAG CTG GCG ATT GCT CAT TCT GCC GAC CAG CAG Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln	640	645	672
GGC CTG AAC GGC GGC CAG ATG GGC TGG GGC CGT ATT CAG GAG TTG CCC Ala Leu Asn Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro	655	660	720
GGG ATC TTC GCC CAG GCA TTA AGC ACC GCG AAG AAA GGC GAC ATT GTT Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val	670	675	768
GGC CCG ATT CGT TCC GGC GTT GGC TTC CAT ATT CTG AAA GTT AAC GAC Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp	685	690	816
CTG CGC GGC GAA AGC AAA AAT ATC TCG GTG ACC GAA GTT CAT GCT CGC			864

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Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg	
700 705 710 715	
CAT ATT CTG CTG AAA CCG TCG CCG ATC ATG ACT GAC GAA CAG GCC CGT	912
His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg	
720 725 730	
G TG AAA CTG GAA CAG ATT GCT GCT GAT ATC GAG AGT GGT AAA ACG ACT	960
Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr	
735 740 745	
TTT GCT GCC GCA ACG AAA GAG TTC TCT CAG GAT CCA GTC TCT GCT AAC	1008
Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn	
750 755 760	
CAG GGC GGC GAT CTC GGC TGG GCT ACA CCA GAT ATT TTC GAT CCG GCC	1056
Gln Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala	
765 770 775	
TTC CGT GAC GCC CTG ACT CGC CTG AAC AAA GGT CAA ATG AGT GCA CCG	1104
Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro	
780 785 790 795	
GTT CAC TCT TCA TTC GGC TGG CAT TTA ATC GAA CTG CTG GAT ACC CGT	1152
Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg	
800 805 810	
AAT GTC GAT AAA ACC GAC GGT GCG CAG AAA GAT CGT GCA TAC CGC ATG	1200
Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met	
815 820 825	
CTG ATG AAC CGT AAG TTC TCG GAA GAA GCA GCA AGC TGG ATG CAG GAA	1248
Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu	
830 835 840	
CAA CGT GCC AGC GCC TAC GTT AAA ATC CTG AGC AAC TAA	1287
Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn	
845 850 855	

*(2)* INFORMATION FOR SEQ ID NO: 4:

- (i)* SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 428 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii)* MOLECULE TYPE: protein
- (xi)* SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn	
1 5 10 15	
Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val	
20 25 30	

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser  
 35 40 45

Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala  
 50 55 60

Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile  
 65 70 75 80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu  
 85 90 95

Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp  
 100 105 110

Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr  
 115 120 125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn  
 130 135 140

Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu  
 145 150 155 160

Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu  
 165 170 175

Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val  
 180 185 190

Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn  
 195 200 205

Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln  
 210 215 220

Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro  
 225 230 235 240

Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val  
 245 250 255

Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp  
 260 265 270

Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg  
 275 280 285

His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg  
 290 295 300

Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr  
 305 310 315 320

Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn

325

330

335

Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala  
340 345 350

Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro  
355 360 365

Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg  
370 375 380

Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met  
385 390 395 400

Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu  
405 410 415

Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn  
420 425

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